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OM protein - protein search, using sw model
Run on: October 26, 2002, 21:05:33 ; Search time 27 Seconds
(without alignments)
1480.068 Million cell updates/sec

SUMMARIES

Db	61	CITCAVAINRQKVNCATTSNAVCGDCLPFRYRKTRIGGLQDQCICPCTKQTPTSEVOCAF	RN [1]
RP		SEQUENCE FROM N.A.	
RA		Chaudhary D., Long A.J.;	
RT		"TRANE, a novel TNF receptor family member associated with death signalin";	
RL		Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
DR		EMBL; AF246998; AAC28395.1; -.	
DR		InterPro; IPR01368; TNFR_c6.	
DR		Pfam; PF0000; TNFR_c6; 2.	
DR		SMART; SMC0208; TNFR_c6; 2.	
DR		PROSITE; FS0052; TNFR_NGFR_1; UNKNOWN_2.	
DR		PROSITE; FS0050; TNFR_NGFR_2; 1.	
SQ		SEQUENCE FROM N.A.	
09NZV2		PRELIMINARY; PRT; 423 AA.	
ID	09NZV2		
AC	09NZV2;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DE	TAJ-ALPHA.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP		SEQUENCE FROM N.A.	
RX		MEDLINE=20270246; PubMed=10809768;	
RA		EBI_M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;	
RT		"TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death."; 275:15336-15342(2000).	
RT		J. Biol. Chem. 275:15336-15342(2000).	
RL		EMBL; AF167555; AAT71828.1; -.	
DR		InterPro; IPR01368; TNFR_c6.	
DR		Pfam; PF00020; TNFR_c6; 2.	
DR		SMART; SM00208; TNFR_c6; 2.	
DR		PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.	
DR		PROSITE; PS0050; TNFR_NGFR_2; 1.	
SEQUENCE	423 AA;	46071 MW;	BB7991713A4B2F CRC64;
Query Match	38.1%; Score 485; DB 4; Length 417; Best Local Similarity 44.9%; Pred. No. 5e-44; Matches 29; Mismatches 87; Indels 0; Gaps 0;		
Matches	29; Mismatches 87; Indels 0; Gaps 0;		
DBQ	DCQENEYWDQGRWCYTCQRCGPQGOELSKDCGYGGDAYCTACPERRYKSSWGHHKCOSC 61	QY	2 DCQENEYWDQGRWCYTCQRCGPQGOELSKDCGYGGDAYCTACPERRYKSSWGHHKCOSC 61
Db	33 DCRQEFRDRSGNCVPCNQCGPMELSKEGFGYEDAQCYTCRHRKFEDWGFCKPC 92	Db	33 DCRQEFRDRSGNCVPCNQCGPMELSKEGFGYEDAQCYTCRHRKFEDWGFCKPC 92
QY	62 ITCAVINRQKVNCATTSNAVCGDCLPFRYRKTRIGGLQDQCICPCTKOPTSEVOCAF	QY	62 ITCAVINRQKVNCATTSNAVCGDCLPFRYRKTRIGGLQDQCICPCTKOPTSEVOCAF 121
Db	93 LDCAVVNRFQKANCATSDAICGDCICLPGFYRKTKLVGFQDMECVPCGDPPPYEPHCASK 152	Db	93 LDCAVVNRFQKANCATSDAICGDCICLPGFYRKTKLVGFQDMECVPCGDPPPYEPHCASK 152
QY	122 LSIVEDAAPTVPQEAVALVSSLVFTLAFLGFLFLYCKQFFNRHRCORGGLQFED 181	QY	122 LSIVEDAAPTVPQEAVALVSSLVFTLAFLGFLFLYCKQFFNRHRCORGGLQFED 181
Db	153 VNLVKIASTASSPRDATALAAVICASALAVLLALILCIVLYCKRQFMEKPSWSLRSPQIO 212	Db	153 VNLVKIASTASSPRDATALAAVICASALAVLLALILCIVLYCKRQFMEKPSWSLRSPQIO 212
QY	182 KTAKEESLFPVPSKE 197	QY	182 KTAKEESLFPVPSKE 197
Db	213 YNGSELSCFDRPOLHE 228	Db	213 YNGSELSCFDRPOLHE 228
RESULT	3		
Q9BY00		PRELIMINARY; PRT; 417 AA.	
ID	Q9BY00		
AC	Q9BY00;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	TRADELRH.		
DR		01-OCT-2001 (TREMBLrel. 18, Last annotation update)	
DR		01-OCT-2001 (TREMBLrel. 18, Last annotation update)	
DR		PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.	
DR		PROSITE; PS0050; TNFR_NGFR_2; 1.	
SEQUENCE	423 AA;	46015 MW;	B5891CEA9ED45361 CRC64;
Query Match	37.9%; Score 483; DB 4; Best Local Similarity 44.9%; Pred. No. 8.2e-44; Matches 29; Mismatches 87; Indels 0; Gaps 0;		
Matches	29; Mismatches 87; Indels 0; Gaps 0;		
DBQ	2 DCQENEYWDQGRWCYTCQRCGPQGOELSKDCGYGGDAYCTACPERRYKSSWGHHKCOSC 61	QY	2 DCQENEYWDQGRWCYTCQRCGPQGOELSKDCGYGGDAYCTACPERRYKSSWGHHKCOSC 61
Db	33 DCRQEFRDRSGNCVPCNQCGPMELSKEGFGYEDAQCYTCRHRKFEDWGFCKPC 92	Db	33 DCRQEFRDRSGNCVPCNQCGPMELSKEGFGYEDAQCYTCRHRKFEDWGFCKPC 92

QY 62 ITCAVINRQVKINCTATSNAVCGDCUPFRYKTRIGLQDQCICPCTKQPTSEVOCAFQ 121
 : ||:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 DB 93 LDCAVVNRFORKANSATSDAIGCDCLPGFYRKTKLVGFQDMECVCPGDPPPPYPHCASK 152
 QY 122 LSIVEADAPTVPQEATLVALVSSLLVVFTLAFLGLFLFLYCKQFFNRHCOQGGLIQFEAD 181
 : ||:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 DB 153 VNLVKIATASSPRDTALAAVICSALATVLLALLILCIVICKRQFMEKKPSWSLRQDIO 212
 QY 182 KTAKESELFPVPPSKE 197
 DR 213 YNGSELSCFDRLPQH 228

RESULT 5

Q9BXZ9 PRELIMINARY; PRT; 423 AA.

ID Q9BXZ9 ID: 01-JUN-2001 (TREMBREL. 17, Created)
 AC 01-JUN-2001 (TREMBREL. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBREL. 18, Last annotation update)

DR TRADETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chaudhary D., Long A.J.;
 RT "TRADE, a novel TNF receptor family member associated with death
 signaling.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AF246999; RAK28396; IPR01368; TNFR_c6.
 DR pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM0052; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE; PS0050; TNFR_NGFR_2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 423 AA; 45979 MW; 46D56E41A8A96BA2 CRC64;

Query Match 37.5%; Score 478; DB 11; Length 348;
 Best local Similarity 40.4%; Pred. No. 2. 3e-43;
 Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;

QY 62 DCQENEYWDQNCRCVTCQRCGGQELSKDCGYEGEDAYCTACPPRYKSSWGHHKCOSC 61
 DB 33 DCRQQEFDKDRSGNCVLCQKQCGPMELSKRCGKGYGEDAQCVPCRPHRFKEDMGFQKPC 92
 QY 62 ITCAVINRQVKINCTATSNAVCGDCUPFRYKTRIGLQDQCICPCTKQPTSEVOCAFQ 121
 DB 93 ADCALVNRFORANCSHTSDAVGCDCLPGFYRKTKLVGFQDMECVCPGDPPPPYPHCASK 152
 QY 122 LSIVEADAPTVPQEATLVALVSSLLVVFTLAFLGLFLFLYCKQFFN----- 167
 DB 153 VNLVKIATASSPRDTALAAVICSALATVLLALLILCIVICKRQFMEKKPSWSLRQDIO 212
 QY 168 -----RHCGGGLIQFEAD 181
 DB 213 YNGSELSCFDQLRLHCAHRACCOYHRD 240

RESULT 6

Q9JH6 PRELIMINARY; PRT; 416 AA.

ID Q9JH6 ID: 01-OCT-2000 (TREMBREL. 15, Created)
 AC 01-OCT-2000 (TREMBREL. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBREL. 17, Last annotation update)

DR TROY ("TRADE").
 DE GN TNFRSF19 OR TROY.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20347167; Pubmed=10764796;
 RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 RA Senba E., Kitamura T.,
 RT "TROY, a newly identified member of the tumor necrosis factor receptor
 superfamily, exhibits a homology with Edar and is expressed in
 embryonic skin and hair follicles";
 RT J. Biol. Chem. 275:20742-20747(2000).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Chaudhary D., Long A.J.;
 RT "TRADE, a novel TNF receptor family member associated with death
 signaling.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AB040432; BAB0267; IPR01368; RAK28397; IPR01368;
 DR EMBL; AF247000; RAK28397; IPR01368; TNFRSF19.
 DR MGI; MGI:1352474; TNFRSF19.
 DR InterPro; IPR001368; TNFR_c6.
 DR pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;

Query Match 37.5%; Score 478; DB 11; Length 416;

ID	Best Local Similarity	Pred. No.	2.8e-43;
Matches	84;	Conservative	30;
	Mismatches	66;	Indels 28;
			Gaps 1;
RESULT 8			
OJLL3	PRELIMINARY;	PRT;	416 AA.
09JLL3			
09JLL3; 01-OCT-2000 (TREMBrel. 15, Created)			
01-OCT-2000 (TREMBrel. 15, Last sequence update)			
01-JUN-2001 (TREMBrel. 17, Last annotation update)			
TJ1-ALPHA LONG.			
TNFRSF19.			
Mus musculus (Mouse)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;			
NCBI_TaxID=10090;			
SEQUENCE FROM N.A.			
[2]			
RN			
RP			
SEQUENCE FROM N.A.			
RX			
MEDLINE=20347167; PubMed=10764796;			
RA			
Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A., Senba E., Kitaamra T.,			
"TROY - a newly identified member of the tumor necrosis factor receptor superfamily exhibits a homology with Edar and is expressed in embryonic skin and hair follicles";			
RT			
J. Biol. Chem. 275:20742-20747(2000).			
RL			
J. Biol. Chem. 275:20742-20747(2000).			
RESULT 9			
OJLL3	PRELIMINARY;	PRT;	214 AA.
09JLL3; 01-OCT-2000 (TREMBrel. 15, Created)			
01-OCT-2000 (TREMBrel. 15, Last sequence update)			
01-JUN-2001 (TREMBrel. 17, Last annotation update)			
TJ1-ALPHA LONG.			
TNFRSF19.			
Mus musculus (Mouse)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;			
NCBI_TaxID=10090;			
SEQUENCE FROM N.A.			
[2]			
RN			
RP			
SEQUENCE FROM N.A.			
RX			
MEDLINE=20720246; PubMed=10809768;			
RA			
EBY M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.; RT			
"TJ1, a Novel Member of the Tumor Necrosis Factor Receptor Family", Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death";			
RT			
J. Biol. Chem. 275:15336-15342(2000).			
RL			
J. Biol. Chem. 275:15336-15342(2000).			
DR			
EMBL; AB00433; BAB03268_1; -.			
DR			
EMBL; AF16753; AAFT1826_1; -.			
DR			
MGD; MGII:1352474; Tnfrsf19.			
DR			
InterPro; IPR001368; TNFR_C6.			
DR			
Pfam; PF00020; TNFR_C6; 2.			
DR			
SMART; SM00208; TNFR_2.			
DR			
PROSITE; PS00552; TNFR_NGFR_1; UNKNOWN_2.			
DR			
PROSITE; PS00550; TNFR_NGFR_2; 1.			
DR			
SEQUENCE 214 AA; 2356 MW; EC63981; C37482B8 CRC64;			
Query Match	37.5%	Score 478;	DB 11; Length 214;
Best Local Similarity	47.9%	Pred. No. 3.6e-43;	
Matches	79;	Conservative	29;
	Mismatches	57;	Indels 0;
			Gaps 0;
QY			
2 DCQENEYWDQWGRGVTCORCGPGSLELSKCGYERGGDAVCTACPPRRKSSWQHHKOSC 61			
33 DCQROEFKDRSGNCVLCCKQGPMLSKCGFGYGEDAQCPVRPHRFEDMGFQKCPK 92			
62 ITCAVINVRYKVNCTATSAVQGDCCLPFRYKRIGGLQDQECPCTQQTPTSEVQCAFO 121			
93 ADCALVNRFORANGCSHTSDAVCCDCCLPQGPYRKRIGLKVQDMEVCPGCPPPPPEPHCISK 152			
122 LSLVEADAPTVPOEATVALVSSLVVFATLAFGLFLYCKOFF----- 167			
153 VNLYKISSVSSPRDTALAAVICASALATVLLALILCIVIYCKQFMEKKPSWSLRSDQIQ 212			
168 -----RHCQRGGLIQLEAD 181			
213 YNGSELSCFDQPRURHCAHRACQYHRD 240			
RESULT 10			
OJLL2	PRELIMINARY;	PRT;	150 AA.
09JLL2; 01-OCT-2000 (TREMBrel. 15, Created)			
01-OCT-2000 (TREMBrel. 15, Last sequence update)			
01-JUN-2001 (TREMBrel. 17, Last annotation update)			
TJ1-BETA1.			
TNFRSF19.			
Mus musculus (Mouse)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;			
NCBI_TaxID=10090;			
SEQUENCE FROM N.A.			
RX			
MEDLINE=20720246; PubMed=10809768;			
RA			
EBY M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M., RT			
"TJ1, a Novel Member of the Tumor Necrosis Factor Receptor Family",			

OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99364417; PubMed=10311242;
 RA Heodon D.J.; Overbeeck P.A.;
 RT "Involvement of a novel tnf receptor homologue in hair follicle
 induction.";
 RL Nat. Genet. 22:370-374(1999).
 DR EMBL; AR160502; AAD50425.1; -.
 DR MGI; MGI:1343498; Edar.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 KW Receptor.
 SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;
 SQ

Query Match 14.4%; Score 183.5; DB 11; Length 448;

Best Local Similarity 25.0%; Pred. No. 1.9e-11; Indels 59; Gaps 13; Matches 70; Conservative 29; Mismatches 59; Gaps 13;

QY 2 DCEPENEWWDQ-WRCVCVWCQRCPGQELSKDKCGYEGEDAY-CTACPPRKYSSWMGHKCOS 60
 Db 30 NCGENEYHNOTQNLGCQQCPCRGEEPEPMSCGCGTKKDDYGCVPCKAEFSKGQYICRR 89
 QY 55 HKHQCSCTCAVINRVKVNCTATSNAVCGDGLPFRY-KRIGGLQDQECLPCTKQTPT 113
 Db 90 HKDCGEFRATVLTGPDMEN---DAECGPCLPGTYMLNRPNITYGMVYCSSLAPPN 144
 QY 114 SWOCAFQLSLVEDA----PTVPOE-----ATLVAVLSSLLVFTLAFLGLFLFLYCK 155
 Db 145 TK-ECVGATSGSYSAHSSTSSTGGSTLSFPQAHKEKLSQGHALATLITAMSTIFIMAIV 203
 QY 156 GLFFLY--CKOFFNRHCORGGLLOFAADKTAKEESLFPV-----PSKE 197
 Db 204 LIMFVYIMTKTSFSSAPCCSSPPGKSADAPANHEEKREAPDSVWTPENGEFKQLTATPT 263
 QY 196 KTPSAESEQSVSWAGSIAQQLFS---LDSVPVPOQQGPEM 231
 Db 264 KTPKSENDAS--SENEQLLRSVSDDEEPAKDQGSPEL 300

RESULT 14
 ID 090VY2 PRELIMINARY; PRT; 514 AA.

AC 090VY2; DT 01-DEC-2001 (TREMBrel. 19, created)
 DT 01-DEC-2001 (TREMBrel. 19, last sequence update)
 DE ECTODYSPLASIN-A RECEPTOR.

QY 3 COENYEWWDQGR-CVTCVCGPGQELSKDKCGYEGEDAY-CTACPPRKYSSWMGHKCOS 60
 Db 32 CGEYEFFNQINSQACPCPQGPQEPNMSCHGKMDGECFACVPCPQGY-SKGKYEICRR 90

QY 61 CITEC-AVINVVKVNCTATSNAVCGDGLPFRY-KRIGGLQDQECLPCTKQTPTSEVQ 118

Db 91 HKDCNALYKATVRIEPTAEDKARCGPCLPGYYMENRARNLYAMCHSC-ONAPLNTEC 149
 QY 119 AFQL-----SLVENDATPVPPQEAETLVAVLSSLLVFTLA---FLGLFLFLYCK 163
 Db 150 KTTTEPIIKPPINGSTVLPHGGSPGQGHALATLITAMSTIFIMAIVLIMFYKA 209

QY 164 QFFNRHCORGGLQFEADKTAKEESLFPV-----PSKE 197
 Db 210 KPNQOACCSGGVVKAVEOTINKLEDKKDVDPDNVVIFPEKE 249

RESULT 15
 ID 090Z36 PRELIMINARY; PRT; 514 AA.

AC 090Z36; DT 01-DEC-2001 (TREMBrel. 19, created)
 DT 01-DEC-2001 (TREMBrel. 19, last sequence update)
 DE ECTODYSPLASIN-A RECEPTOR.

QY 1 Oryzias latipes (Medaka fish).
 Db 2 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belioniformes; Adrianichthyidae; Oryziinae; Oryzias.
 RN [1]
 RP STRAIN=NHL;
 RA Kondo S.; Shima A.;
 RT "The medaka rs-3 locus required for scale development encodes
 ectodysplasin-A receptor";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF364815; AAK83298.1; -.
 KW Receptor.

SQ SEQUENCE 514 AA; 56074 MW; 8389E28082738632 CRC64;

Query Match 12.9%; Score 164.5; DB 13; Length 514;
 Best Local Similarity 25.5%; Pred. No. 2.5e-09;
 Matches 56; Conservative 34; Mismatches 103; Indels 27; Gaps 9;

QY 3 COENYEWWDQGR-CVTCVCGPGQELSKDKCGYEGEDAY-CTACPPRKYSSWMGHKCOS 60
 Db 32 CGEYEFFNQINSQACPCPQGPQEPNMSCHGKMDGECFACVPCPQGY-SKGKYEICRR 90

QY 61 CITEC-AVINVVKVNCTATSNAVCGDGLPFRY-KRIGGLQDQECLPCTKQTPTSEVQ 118

Db 91 HKDCNALYKATVRIEPTAEDKARCGPCLPGYYMENRARNLYAMCHSC-ONAPLNTEC 149
 QY 119 AFQL-----SLVENDATPVPPQEAETLVAVLSSLLVFTLA---FLGLFLFLYCK 163
 Db 150 KTTTEPIIKPPINGSTVLPHGGSPGQGHALATLITAMSTIFIMAIVLIMFYKA 209

SEARCH completed: October 26, 2002, 21:09:48
 Job time : 30 secs

Query Match 13.1%; Score 166.5; DB 13; Length 514;
 Best Local Similarity 24.5%; Pred. No. 1.5e-09;
 Matches 54; Conservative 38; Mismatches 101; Indels 27; Gaps 9;

KW Receptor.
 RC SEQUENCE 514 AA; 56066 MW; 82C7F0661EFCFB48 CRC64;

RQ The medaka rs-3 locus required for scale development encodes ectodysplasin-A receptor;
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.